

GAATTCAGTGTGCTGGCTTCC) .CTGCAGCACAGCACACTCCCTTGGCAAGGACCTGAGACCCCTTGTG. .GTC

1
AAGAGGCTCAATGGGCTGCAGAAGAACTAGAGAAGGACCAAGCAAAGCC met ile phe pro trp lys [cys
ATG ATA TTT CCA TGG AAA TGT]

10
gln ser thr gln arg asp leu trp asn ile phe lys [cys
CAG AGC ACC CAG AGG GAC TTA TGG AAC ATC TTC AAG TTT TGG GGG TGG ACA ATG CTC TGT]

20
Signal Sequence
leu trp gly trp thr met leu [cys
TTG TGG GGG TGG ACA ATG CTC TGT]

30
asp phe leu ala [cys
GAT TTC CTG GCA] his his gly thr tyr [cys
CAT CAT GGA ACC TAC TGC] trp thr tyr his tyr ser glu lys pro
TGG ACT TAC CAT TAT TCT GAA AAA CCC

40
Probable N-Terminus
met asn trp gln arg ala arg arg phe [cys
ATG AAC TGG CAA AGG GCT AGA AGA TTC TGC] arg asp [asn tyr thr] asp leu val ala ile
AAT TAC ACA GAT TTA GTT GCC ATA

50
gln asn lys ala glu ile glu tyr leu glu lys thr leu pro phe ser arg ser tyr tyr
CAA AAC AAG CGG GAA ATT GAG TAT CTG GAG AAG ACT CTG CCC TTC AGT CGT TCT TAC TAC

60
trp ile gly ile arg lys ile gly gly ile trp thr trp val gly thr [asn lys ser] leu
TGG ATA GGA ATC CGG AAG ATA GGA GGA ATA TGG ACG TGG GTG GGA ACC AAC AAA TCT CTC

70
thr glu glu ala glu asn trp gly asp gly glu pro [asn lys lys] asn lys glu asp
ACT GAA GAA GCA GAG AAC TGG GGA GAT GGT GAG CCC AAC AAC AAG AAG AAC AAG GAG GAC

80
[cys] val glu ile tyr ile lys arg asn lys asp ala gly lys trp asn asp asp ala [cys
TGC GTG GAG ATC TAT ATC AAG AGA AAC AAA GAT GCA GGC AAA TGG AAC GAT GAC GCC TGC]

90
his lys leu lys ala ala leu [cys] tyr thr ala ser [cys] gln pro trp ser [cys] ser gly
CAC AAA CTA AAG GCA GCC CTC TGT TAC ACA GCT TCT TGC CAG CCC TGG TCA TGC AGT GGC

100
his gly glu [cys] val glu ile ile asn [asn his thr] [cys] [cys] asp val gly tyr tyr
CAT GGA GAA TGT GTA GAA ATC ATC AAT AAT CAC ACC TGC AAC TGT GAT GTG GGG TAC TAT

110
gly pro gln [cys] gln leu val ile gln [cys] glu pro leu glu ala pro glu leu gly thr
GGG CCC CAG TGT CAG CTT GTG ATT CAG TGT GAG CCT TTG GAG GCC CCA GAG CTG GGT ACC

120
met asp [cys] thr his pro phe gly [asn phe ser] phe ser ser gln [cys] ala phe ser [cys]
ATG GAC TGT ACT CAC CCC TTT GGA AAC TTC AGC TTC AGC TCA CAG TGT GCC TTC AGC TGC

130
ser glu gly thr [asn leu thr] gly ile glu glu thr thr [cys] gly pro phe gly [asn trp]
TCT GAA GGA ACA AAC TTA ACT GGG ATT GAA GAA ACC ACC TGT GGA CCA TTT GGA AAC TGG

140
[ser] ser pro glu pro thr [cys] gln val ile gln [cys] glu pro leu ser ala pro asp leu
TCA TCT CCA GAA CCA ACC TGT CAA GTG ATT CAG TGT GAG CCT CTA TCA GCA CCA GAT TTG

150
gly ile met [asn [cys] ser] his pro leu ala ser phe ser phe thr ser ala [cys] thr phe
GGG ATC ATG AAC TGT AGC CAT CCC CTG GCC AGC TTC AGC TTT ACC TCT GCA TGT ACC TTC

160
ile [cys] ser glu gly thr glu leu ile gly lys lys lys thr ile [cys] glu ser ser gly
ATC TGC TCA GAA GGA ACT GAG TTA ATT GGG AAG AAG AAA ACC ATT TGT GAA TCA TCT GGA

170
ile trp ser [asn pro ser] pro ile [cys] gln lys leu asp lys ser phe ser met ile lys
ATC TGG TCA AAT CCT AGT CCA ATA TGT CAA AAA TTG GAC AAA AGT TTC TCA ATG ATT AAG

180
Stop Transfer Sequence
glu gly asp tyr asn pro leu phe ile pro val ala val met val thr ala phe ser gly
GAG GGT GAT TAT AAC CCC CTC TTC ATT CCA GTG GCA GTC ATG GTT ACT GCA TTC TCT GGG

190
leu ala phe ile ile trp leu ala arg arg leu lys lys gly lys lys ser lys arg ser
TTG GCA TTT ATC ATT TGG CTG GCA AGG AGA TTA AAA AAA GGC AAG AAA TCC AAG AGA AGT

200
met asn asp pro tyr OC
ATG AAT GAC CCA TAT TAA ATCGCCCTTGGTGAAGAAATTCCTTGAATACTAAAAATCATGAGATCCTTTA
AATCCTTCCATGAACGTTTGTGTGGTGGCACCTCTACGTCAACATGAAGTGTGTCTCTCAGTGCATCTGGGAA
GATTTCACCCGACCAACAGTTCTTTCAGCTTCCATTTTCCCTCAACCCCGAGCCACAGGTGTT
TATACAGCTCAGCTTTTGTCTTTTCTGAGGAGAAACAAATAAGACCATAAGGGAAAGGATTTCATGTGGAATATAAG
ATGGCTGACITTGCTCTTTCTTCTGACTCTTGTCTTTCAGTTTCAATTCAGTCTCTACTTCATGACAGACACTTCTAAT
GAAGTGCAAAATTTGATACATATGTGAATATGGACTCAGTTTTCTTGAGATCAAAATTCAGTCTCTTCTGTATACT
GTGGAGGTACACTCTTATAGAAAGTTCAAAAGTCTACGCTCTCTCTTCTTCTAATCCAGTGAAGTAATGGGTCC
TGCTCAAGTTGAAGAGTCTTATTTGCACTGTAGCCTCGCCGTCTGTGAATTGGACCATCTATTTAATCGGCTCAG
GCCTCCCCACCTTCTTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATGAGTGCCAAAGCAA
AAGGAGAGAAGAGAGAAATAGCCTCGCGCGTTTTTAGTTTGGGGTTTTGCTGTTTCTTTTATGAGACCCATTCTCT
ATTTCTTATAGTCAATGTTTCTTTTATCAGGATATTATTAGTAAGAAAACATCACTGAAATGCTAGCTGCAAGTGACA
TCTCTTTGATGTATATGGAAGAGTTAAACAGGTGGAGAAATTCCTTGATTACAAATGAAATGCTCTCTTTCCCT
GCCCCAGAACTTTTATCCACTTACCTAGATTCTACATATTTTAAATTCATCTCAGGCTCTCTCAACCCACGG
GGCCGCCAGCACACTGGAATTC

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Fig. 1

Fig. 2

GAATTCGAGCTCGTCGACCACGCCCTCTTGTGCAAGAACTCTGAGCCCCAGGTGCAGGAGGCTGAGGCTGCATAG

1 10
met val phe pro trp arg [cys] glu gly thr tyr trp gly
ATG GTG TTT CCA TGG AGA [TGT] GAG GGT ACT TAC TGG CCC

20 30
ser arg asn ile leu lys leu trp val trp thr leu leu [cys] [cys] asp phe leu ile his
TCG AGG AAC ATC CTG AAG [CTG TGG GTC TGG ACA CTG CTC [TGT] [TGT] GAC TTC CTG ATA] CAC

40 50
N-Terminus
his gly thr his [cys] trp thr tyr his tyr ser glu lys pro met asn trp glu asn ala
CAT GGA ACT CAC [TGT] TGG ACT TAC CAT TAT TCT GAA AAG CCC ATG AAC TGG GAA AAT CCT

60 70
arg lys phe [cys] lys gln [asn tyr thr] asp leu val ala ile gln asn lys arg glu ile
AGA AAG TTC [TGT] AAG CAA [AAT TAC ACA] GAT TTA GTC GCC ATA CAA AAC AAG AGA CAA ATT

80 90
glu tyr leu glu asn thr leu pro lys ser pro tyr tyr trp ile glu ile arg lys
GAG TAT TTA GAG AAT ACA TTG CCC AAA AGC CCT TAT TAC TAC TGG ATA GGA ATC AGC AAA

100 110
ile gly lys met trp thr trp val gly thr [asn lys thr] leu thr lys glu ala glu asn
ATT GCG AAA ATG TGG ACA TGG CTG GCA ACC [AAC AAA ACT] CTC ACT AAA GAA GCA GAG AAC

120 130
trp gly ala gly glu pro asn asn lys lys ser lys glu asp [cys] val glu ile tyr ile
TGG GGT GCT GCG GAG CCC AAC AAC AAG AAG TCC AAG GAG GAC [TGT] GTC GAG ATC TAT ATC

140 150
lys arg glu arg asp ser gly lys trp asn asp asp ala [cys] his lys arg lys ala ala
AAG AGC GAA CCA GAC TCT GCG AAA TGG AAC GAT GAC GCC [TGT] CAC AAA CCA AAG GCA GCT

160 170
leu [cys] tyr thr ala ser [cys] gln pro gly ser [cys] asn gly arg gly glu [cys] val glu
CTC [TGT] TAC ACA GCC TCT [TGT] CAG CCA GGG TCT [TGT] AAT GCG CGT GCA GAA [TGT] GTC GAA

180 190
thr ile asn [asn his thr] [cys] ile [cys] asp ala gly tyr tyr gly pro gln [cys] gln tyr
ACT ATC AAC [AAT CAC ACG] [TGT] ATC [TGT] GAT GCA GCG TAT TAC GCG CCC CAG [TGT] CAG TAT

200 210
val val gln [cys] glu pro leu glu ala pro glu leu gly thr met asp [cys] ile his pro
GTG GTC CAG [TGT] GAG CCT TTG GAG CCC CCT GAG TTG GGT ACC ATG GAC [TGT] ATC CAC CCC

220 230
leu gly [asn phe ser] phe gln ser lys [cys] ala phe [asn cys ser] glu gly arg glu leu
TTG GGA [AAC TTC AGC] TTC CAG TCC AAG [TGT] GCT TTC [AAC TGT TCT] GAG GGA AGA GAG CTA

240 250
leu gly thr ala glu thr gln [cys] gly ala ser gly [asn trp ser] ser pro glu pro ile
CTT GCG ACT GCA GAA ACA CAG [TGT] GGA GCA TCT GGA [AAC TGG TCA] TCT CCA GAG CCA ATC

260 270
[cys] gln val val gln [cys] glu pro leu glu ala pro glu leu gly thr met asp [cys] ile
[TGT] CAA GTG GTC CAG [TGT] GAG CCT TTG GAG GCC CCT GAG TTG GGT ACC ATG GAC [TGT] ATC

280 290
his pro leu gly [asn phe ser] phe gln ser lys [cys] ala phe [asn cys ser] glu gly arg
CAC CCC TTG GGA [AAC TTC AGC] TTC CAG TCC AAG [TGT] GCT TTC [AAC TGT TCT] GAG GGA AGA

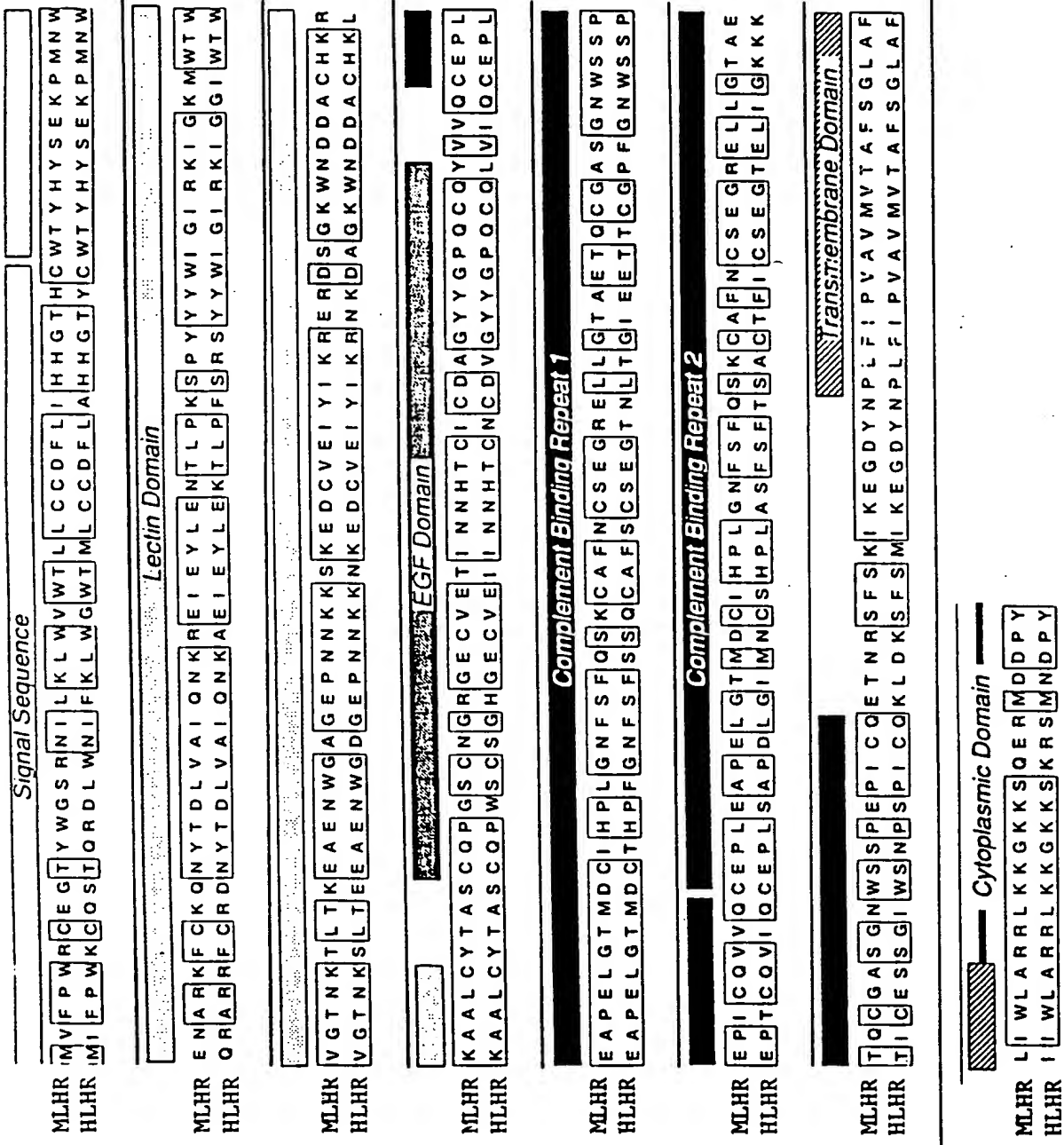
300 310
glu leu leu gly thr ala glu thr gln [cys] gly ala ser gly [asn trp ser] ser pro glu
GAG CTA CTT GCG ACT GCA GAA ACA CAG [TGT] GGA GCA TCT GGA [AAC TGG TCA] TCT CCA GAG

320 330
pro ile [cys] gln glu thr [asn arg ser] phe ser lys ile lys glu gly asp tyr asn [pro]
CCA ATC [TGT] CAA GAG ACA [AAC AGA AGT] TTC TCA AAG ATC AAA GAA GGT GAC TAC AAC [CCC]

340 350
Stop Transfer Sequence
leu phe ile pro val ala val met val thr ala phe ser gly leu ala phe leu ile trp
CTC TTC ATT CCT GTA GCG GTC ATG GTC ACC GCA TTC TCG GCG CTG GCA TTT CTC ATT TCG

360 370 372
leu ala arg arg leu lys lys gly lys ser gln glu arg met asp asp pro tyr OP
[TGT GCA] AGG CCG TTA AAA AAA GCG AAG AAA TCT CAA GAA AGG ATG CAT CAT CCA TAC TCA

TTTATCCTTTTGTAAAGGAAGCCATGAAGTCTAAGACAAAACATTCGAAAATAACGTCAAGTCTCTCCGTCAGCA
TTTTACACCGAGGCATCTCCACATATAGAGATGCAGTGTTTGTCTAACGAATCTGGAAGGATTCTTTCATGACCAACA
GCTCTCTAATTTCCCTCGCTCATTCATCCCATTAACCTATCCCATTAATGTGTCTATACAGAGTAGTATTTTA
TCATCTTTTCTGTGGAGGAACAAGCAAAAGTGTACTGTAGAATATAAGACAGCTGCTTTTACTCTTTCCTAATCTCT
TCTTTCTAGTTCAATTCAGCACAGAGCTAATGCCAACACAGTGAATAATGATCCATGAGTAATTCGAAACTCAG
ACTCCTTGGCATAGTACGTACCTATGTAAATCGACAAAATCTTTTCTATTTCCACCTCCAAAGAACAGTCTCTAT
TCAAGTTGGAAAGTCTTCTCTCTGTAGACCCACTATCTGTGAGTGACAGCCACTGTAGCTGTTTACATTAACTT
TCCCATCTCTTTTCTAGGAGAAATAATTCACACACTGCACCCATGATGCGCCACCAACATCAAGCAAGCGAAAA
TCTCTGCATTGAGTTTATGTTTTCAGTTTCTCTTTTATTAGATCTCTGATGCTTCTTGAAGTCAGTCTTCT
GATGATTATTAATAGTTAATGATAACACACACCTCTCTTGGAGCTGATCTTATGAAGACACAGGTAGAAAAATTC
CTGGGCTCAGGCTGCAGTGACACCTTTTCTTTCCCTAACATCTTCTACTCAGATACCTAAATTTAAGATTACGACA
GCTGTCCCCAATCTTACCATGTCTTTTATAACTTGTCTCTTAACCTTGCCEAACCTGTAGGCTATCTCATTTTCTCGC
TTCATCTGCAAGCTTTATAACATGATGAATTTAATACAAAAA



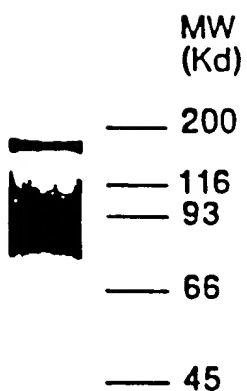


Fig. 4A

Fig. 4B

T H K M K F K V V I L K
 1 10 20 30
 X T Y H Y S E K P M N W E N A R K F X K Q N Y T D L V A I Q N K X X I E Y L

Fig. 4C

A A C A C
 5' GAG AAG CCC ATG AAT TGG GAG AAT GC 3'

Fig. 5

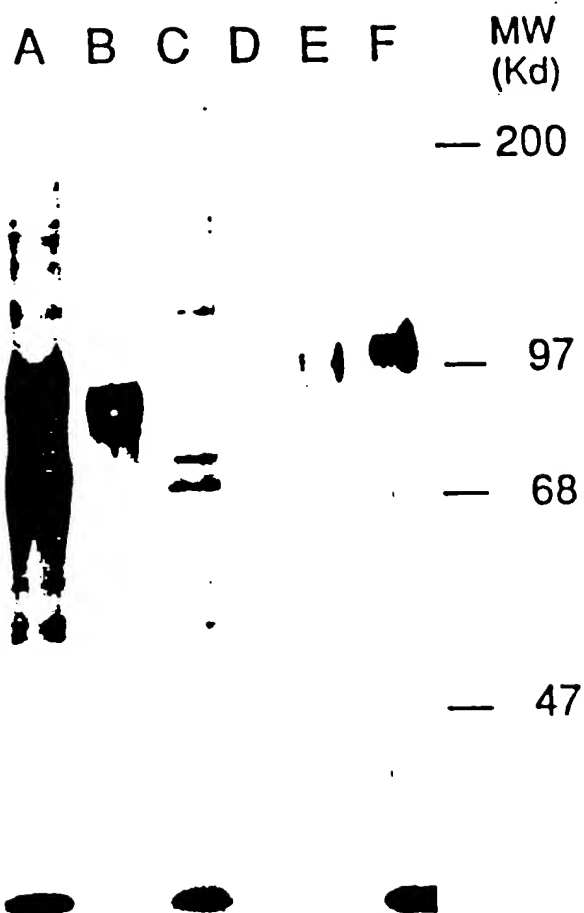


Fig. 6A

[illegible][illegible]

Drickamer		P	G	E	C	C	W	N	D	C	C
MLHR	115	G A G E P N N	K K S K E	D C V E I Y I	K R E R S G K W N D D A C	H K R K A A	L	C			
Hu. HepLec	254	A V T Q P	D N W H G H E	L G G S E D C V E V Q P D	G R W N D D F C	L Q V Y R W	V	C			
Barn. Lec	73	S S N N P N N	- W E N Q	D C G V V N Y	- D T V T G Q W D D D C	N K N K N F	L	C			
Ra. HepLec	194	R P G Q P	D D W Y G H G	- L G G G E D C A H F T T D G	H W N D V C	R R P Y R W	V	C			
Ch. HepLec	136	K E G E P N N	R G F N E	D C A H V W	- - - T S G Q W N D V Y C	T Y E C Y Y	V	C			
Hu. IgErec	194	A P G E P	T S R S Q G E	D C	- - - V M M R G S G R W N D A E C	D R K L G A W V C					
Ra. HepLec2	194	A F T O P	D N C O G H E	- E G G S E D C A E I L S D G L	W N D N F C	Q Q V N R W	A	C			
Ra. ASGrec	194	A F T O P	D N W O G H E	- E G G S E D C A E I L S D G L	W N D N F C	Q Q V N R W	A	C			
Ra. TRP	80	D T G Y P N N	- S N R G	- Y C V S -	V T S N S G Y K K W R D N S C	D A Q L S F	V	C			
Ra. MBP	193	K K D E P N D	H G S G E	- D C V T I	- - - V D N G L W N D I S C	Q A S H T A	V	C			
Ra. MBDA	72	K K D E P N D	H G S G E	- D C V T I	- - - V D N G L W N D I S C	Q A S H T A	V	C			
Ra. KCBP	77	R K G Q P	D N W R H G N	- G E R E D C V H L Q R	- - - M W N D M A C	G T A Y N W	V	C			
FlyLec	84	S E N N P D N	Y K H O E	- H C V H I W	- - D T K P L Y O W N D N D	C N V K M G Y	I	C			
Rab. Surf	75	Y P G E P R G	- Q G R E	- K C V E M Y	- - - T D G K W N D K N C L	Q Y R L V	I	C			

Fig. 6B

MLHR	160	C	Q	P	G	S	C	N	G	R	G	E	C	V	E	T	I	N	N	H	T	C	I	C	D	A	G	Y	Y	G	P	Q	C	Q	Y	
Notch	1021	C	T	E	S	S	C	L	N	G	G	S	C	I	D	G	I	N	G	Y	N	C	S	C	L	A	G	Y	S	G	A	N	C	Q	Y	
S.purp.	61	C	A	S	A	P	C	C	Q	N	G	G	V	C	I	D	G	V	N	G	Y	M	C	C	Q	P	G	Y	T	G	T	H	C	E	T	
Pro.Z	1	C	A	S	Q	P	C	L	N	N	G	S	C	Q	D	S	I	R	G	Y	A	C	T	C	A	P	G	Y	E	G	P	N	C	A	F	
Fact.X	61	C	E	G	H	P	C	L	N	Q	G	H	C	K	D	G	I	G	D	Y	T	C	T	C	A	E	G	F	E	G	K	N	C	E	F	
Fact.VII	61	C	E	T	S	P	C	Q	N	Q	G	K	C	K	D	G	L	G	E	Y	T	C	T	C	L	E	G	F	E	G	K	N	C	E	L	
Fact.IX	1	C	E	S	N	P	C	L	N	G	G	M	C	K	D	D	I	N	S	Y	E	C	W	C	Q	A	G	F	E	G	T	N	C	E	L	
Lin-12	361	C	L	E	N	P	C	S	N	G	G	V	C	H	Q	H	R	E	S	F	S	C	D	C	P	P	G	F	Y	G	N	G	C	E	Q	
Fact.XII	121	C	R	T	N	P	C	L	H	G	G	R	C	L	E	V	E	G	H	R	L	C	H	C	P	P	V	G	Y	T	G	P	F	C	D	V
Mu.egf	841	C	G	P	G	G	C	G	S	H	A	R	C	V	S	D	G	E	T	A	E	C	Q	C	L	K	G	F	A	R	D	G	N	L	C	

Fig. 6c

MLHR
HuComH
MuComH
HuBeta
HuCR1
EBV/C3d
HuC2
HuB
HuC4b
HuC1s
HuC4b
HuDAF
VacSecP

197
1
61
1
241
361
121
61
341
241
1
61
61

C E P L E A P E L G T M D C I H P L G N F S F Q S K C A F N C S E G R E L L G T A E T Q C
P C G H P G D T P F G T F T L T G G N V F E Y G V K A V Y T C N E G Y O L L G E I N Y R E C
P C G H P G D T P F G S F R L A V G S O F E F G A K V V Y T C D D G Y O L L G E I D Y R E C
C T P R V C P F A G I L E N G A V R Y T T F E Y P N T I S F S C N T G F Y L N G A D C A K C
C O P P P D V L H A E R T O R D K D N F S P G O E V F Y S C E P G Y D L R G A A S M R C
E C Q A P P N I L N G O K E D R H M V R F D P G T S I K Y S C N P G Y V L V G E E S I O C
G A G H C P N P G I S L G A V R T G F R E F G H G D K V R Y R C S S N L V L T G S S E R E C
I H C P R P H D F E N G E Y W P R S P Y Y N V S D E I S F H C Y D G Y T L R G S A N R T C
E F C P S P P A L K D G F V O D E G P M E P V G K N V Y T C N E G Y S L I G N P V A R C
E D T P N S V W E P A K A K Y V F R D V V Q I T C L D G E E V E G R V G A T S F Y S T C
1
E V P T R L N S A S L K Q P Y I T Q N Y E P V Q T V V E Y E C R P G Y R R E P S L S P K L T C
I K R R C P S P R D I D N G O L D I G Q V D F G S I T Y S C N S G Y H L I G E S K S Y C E

MLHR
HuComH
MuComH
HuBeta
HuCR1
EBV/C3d
HuC2
HuB
HuC4b
HuC1s
HuC4b
HuDAF
VacSecP

243
47
107
47
205
405
165
105
505
205
17
105
107

W S S P E P I C Q V V Q C E P L E A P E L G T M D C I H P L G N F S F Q S K C A F N C S E G R E L L G T A E T Q C
W T N D I P I C E V V K C L P V T A P E N G K I V S S A M E P D R E Y H F G
W I N D I P L C E V V K C L P V T E L E N G R I V S G A A E T D O E Y Y F G
W S P E L P V C A P I I C P P S I P T F A T L R V Y K P S A G M N S L Y R
W S P A A P T C E V K S C D D F M Q L L N G R V L F P V N L O L G
W T P P V P Q C K V A A C E A T Q R Q L L T K P O H Q E V R
W S G T E P I C R Q P Y S Y D F E D V A P A L Q T S F S H M L G A T N
W S G Q T A I C D N G A G Y C S M P G I P I G T R K V G S O Y R L E
W L V G E M H C Q K I A C V L P V L M D G I Q S H P O K P F Y T V G
W S N S K L K C Q P V D C Q I P E S I E N G K V E D P E S T L F G
W R P S P P T C E K I T C R K P D V S H G E M V S G F G P I Y N Y K
W S T A V E F C K K S C P N P G E I R N G O L D V P G G I L F G
L S M V W N P E A P I C E S V K C Q S P P S I S N G R H N G Y E D F Y T D G

MLHR
HuComH
MuComH
HuBeta
HuCR1
EBV/C3d
HuC2
HuB
HuC4b
HuC1s
HuC4b
HuDAF
VacSecP

203
80
140
90
304
441
207
145
625
324
50
145
140

S K C A F N C S E G T A E T Q C G A S O N W S S P E P I C O E T N R S
Q A V R F V C N S Q Y K I E G D E E M H C S D D G F W S K E K P K C V E I S C K
Q V V R F E C N S Q F K I E G H K E I H C S E N G L W S N E K P R C V E I L C T
D T A V F E C L P Q H A M F G N D T I T N T T H G N W T K L P E C R E V K C P
A K V D E V C D E G F Q L K G S S A S Y C V L A G M E S L W N S V P V C E Q I F C P
P D V N S S C Q E Q Y K L S Q S V Y Q E G Q G T I P W F M E I R L C K E I T C P
P T Q K T K E S L Q R K I O I O R S G H L N L Y L L D C S Q S V S E N D F L I
D S V T Y H C S R Q L T R G S Q R R T C Q E G S W S Q T E P S C O S F M Y
E K V T V S C S Q G M S L E Q P S A F L C G S S L K W S P E M K N A R C V O K E
S V I R Y T C E E P Y Y M E N G C Q Q E Y H C A G N G S W V N E V L Q P E L P K C V
D T I V F K C Q K G F V L R G S S V I H C D A D S K W N P L P E C R E I Y C P
A T I S F S C N T G Y K L F G S T S S F C L I S G S S V Q W S D P P T C Q I V K C P
S V T Y S C N S Q Y S L I G N S G V L C S G S S V Q W S D P P T C Q I V K C P

Fig. 7

PROTEIN MOTIFS IN THE LYMPHOCYTE HOMING RECEPTOR

